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SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.

THE UNIVERSITY OF TOKYO

<120> EphA4 as therapeutic target of PRC and PDACa

<130> ONC-A0413P

<150> US 60/548,335

<151> 2004-02-27

<150> US 60/555,809

<151> 2004-03-24

<160> 23

<170> PatentIn version 3.1

<210> 1

<211> 3468

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

2 / 3 2

&lt;222&gt; (43)..(3003)

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Met Ala Gly Ile

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ttc tat ttc gcc cta ttt tcg tgt ctc ttc ggg att tgc gac gct gtc 102

Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile Cys Asp Ala Val

5

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aca ggt tcc agg gta tac ccc gcg aat gaa gtt acc tta ttg gat tcc 150

Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr Leu Leu Asp Ser

25

30

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aga tct gtt cag gga gaa ctt ggg tgg ata gca agc cct ctg gaa gga 198

Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser Pro Leu Glu Gly

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ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat aca cca atc cga 246

Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn Thr Pro Ile Arg

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60

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acc tac caa gtg tgc aat gtg atg gaa ccc agc cag aat aac tgg cta 294

Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln Asn Asn Trp Leu

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70	75	80	
cga act gat tgg atc acc cga gaa ggg gct cag agg gtg tat att gag 342			
Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg Val Tyr Ile Glu			
85	90	95	100
att aaa ttc acc ttg agg gac tgc aat agt ctt ccg ggc gtc atg ggg 390			
Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Val Met Gly			
105	110	115	
act tgc aag gag acg ttt aac ctg tac tac tat gaa tca gac aac gac 438			
Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Glu Ser Asp Asn Asp			
120	125	130	
aaa gag cgt ttc atc aga gag aac cag ttt gtc aaa att gac acc att 486			
Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys Ile Asp Thr Ile			
135	140	145	
gct gct gat gag agc ttc acc caa gtg gac att ggt gac aga atc atg 534			
Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly Asp Arg Ile Met			
150	155	160	
aag ctg aac acc gag atc cgg gat gta ggg cca tta agc aaa aag ggg 582			
Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu Ser Lys Lys Gly			
165	170	175	180

4 / 3 2

ttt tac ctg gct ttt cag gat gtg ggg gcc tgc atc gcc ctg gta tca        630  
Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile Ala Leu Val Ser

185                          190                          195

gtc cgt gtg ttc tat aaa aag tgt cca ctc aca gtc cgc aat ctg gcc        678  
Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val Arg Asn Leu Ala  
200                          205                          210

cag ttt cct gac acc atc aca ggg gct gat acg tct tcc ctg gtg gaa        726  
Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser Ser Leu Val Glu  
215                          220                          225

gtt cga ggc tcc tgt gtc aac aac tca gaa gag aaa gat gtg cca aaa        774  
Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys Asp Val Pro Lys  
230                          235                          240

atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc att ggc aac tgc        822  
Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro Ile Gly Asn Cys  
245                          250                          260

cta tgc aac gct ggg cat gag gag cggt agc gga gaa tgc caa gct tgc        870  
Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu Cys Gln Ala Cys  
265                          270                          275

aaa att gga tat tac aag gct ctc tcc acg gat gcc acc tgt gcc aag        918  
Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala Thr Cys Ala Lys

5 / 3 2

280

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tgc cca ccc cac agc tac tct gtc tgg gaa gga gcc acc tcg tgc acc 966  
Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala Thr Ser Cys Thr

295

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tgt gac cga ggc ttt ttc aga gct gac aac gat gct gcc tct atg ccc 1014  
Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala Ala Ser Met Pro

310

315

320

tgc acc cgt cca cca tct gct ccc ctg aac ttg att tca aat gtc aac 1062  
Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile Ser Asn Val Asn  
325 330 335 340

gag aca tct gtg aac ttg gaa tgg agt agc cct cag aat aca ggt ggc 1110  
Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln Asn Thr Gly Gly  
345 350 355

cgc cag gac att tcc tat aat gtg gta tgc aag aaa tgt gga gct ggt 1158  
Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys Cys Gly Ala Gly  
360 365 370

gac ccc agc aag tgc cga ccc tgt gga agt ggg gtc cac tac acc cca 1206  
Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val His Tyr Thr Pro  
375 380 385

6 / 3 2

cag cag aat ggc ttg aag acc acc aaa gtc tcc atc act gac ctc cta      1254  
Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile Thr Asp Leu Leu

390                  395                  400

gct cat acc aat tac acc ttt gaa atc tgg gct gtg aat gga gtg tcc      1302  
Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val Asn Gly Val Ser  
405                  410                  415                  420

aaa tat aac cct aac cca gac caa tca gtt tct gtc act gtg acc acc      1350  
Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val Thr Val Thr Thr  
425                  430                  435

aac caa gca gca cca tca tcc att gct ttg gtc cag gct aaa gaa gtc      1398  
Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln Ala Lys Glu Val  
440                  445                  450

aca aga tac agt gtg gca ctg gct tgg ctg gaa cca gat cgg ccc aat      1446  
Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro Asp Arg Pro Asn  
455                  460                  465

ggg gta atc ctg gaa tat gaa gtc aag tat tat gag aag gat cag aat      1494  
Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys Asp Gln Asn  
470                  475                  480

gag cga agc tat cgt ata gtt cgg aca gct gcc agg aac aca gat atc      1542  
Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg Asn Thr Asp Ile

7 / 3 2

485	490	495	500
aaa ggc ctg aac cct ctc act tcc tat gtt ttc cac gtg cga gcc agg      1590			
Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His Val Arg Ala Arg			
505	510	515	
aca gca gct ggc tat gga gac ttc agt gag ccc ttg gag gtt aca acc      1638			
Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu Glu Val Thr Thr			
520	525	530	
aac aca gtg cct tcc cggt atc att gga gat ggg gct aac tcc aca gtc      1686			
Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala Asn Ser Thr Val			
535	540	545	
ctt ctg gtc tct gtc tcg ggc agt gtg gtg ctg gtg gta att ctc att      1734			
Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val Val Ile Leu Ile			
550	555	560	
gca gct ttt gtc atc agc cggt aga cggt agt aaa tac agt aaa gcc aaa      1782			
Ala Ala Phe Val Ile Ser Arg Arg Ser Lys Tyr Ser Lys Ala Lys			
565	570	575	580
caa gaa gcg gat gaa gag aaa cat ttg aat caa ggt gta aga aca tat      1830			
Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly Val Arg Thr Tyr			
585	590	595	

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gtg gac ccc ttt acg tac gaa gat ccc aac caa gca gtg cga gag ttt      1878

Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val Arg Glu Phe

600

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610

gcc aaa gaa att gac gca tcc tgc att aag att gaa aaa gtt ata gga      1926

Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys Val Ile Gly

615

620

625

gtt ggt gaa ttt ggt gag gta tgc agt ggg cgt ctc aaa gtg cct ggc      1974

Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Val Pro Gly

630

635

640

aag aga gag atc tgt gtg gct atc aag act ctg aaa gct ggt tat aca      2022

Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr

645

650

655

660

gac aaa cag agg aga gac ttc ctg agt gag gcc agc atc atg gga cag      2070

Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met Gly Gln

665

670

675

ttt gac cat ccg aac atc att cac ttg gaa ggc gtg gtc act aaa tgt      2118

Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val Thr Lys Cys

680

685

690

aaa cca gta atg atc ata aca gag tac atg gag aat ggc tcc ttg gat      2166

Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp

9 / 3 2

695 700 705

gca ttc ctc agg aaa aat gat ggc aga ttt aca gtc att cag ctg gtg 2214  
Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile Gln Leu Val

710 715 720

ggc atg ctt cgt ggc att ggg tct ggg atg aag tat tta tct gat atg 2262  
Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu Ser Asp Met  
725 730 735 740

agc tat gtg cat cgt gat ctg gcc gca cg<sup>g</sup> aac atc ctg gtg aac agc 2310  
Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser  
745 750 755

aac ttg gtc tgc aaa gtg tct gat ttt ggc atg tcc cga gtg ctt gag 2358  
Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg Val Leu Glu  
760 765 770

gat gat ccg gaa gca gct tac acc acc agg ggt ggc aag att cct atc 2406  
Asp Asp Pro Glu Ala Ala Tyr Thr Arg Gly Gly Lys Ile Pro Ile  
775 780 785

cg<sup>g</sup> tgg act gcg cca gaa gca att gcc tat cgt aaa ttc aca tca gca 2454  
Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser Ala  
790 795 800

10 / 32

agt gat gta tgg agc tat gga atc gtt atg tgg gaa gtc atg tcg tac 2502  
Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr  
805 810 815 820

ggg gag agg ccc tat tgg gat atg tcc aat caa gat gtc att aaa gcc 2550  
Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala  
825 830 835

att gag gaa ggc tat cgg tta ccc cct cca atg gac tgc ccc att gcg 2598  
Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile Ala  
840 845 850

ctc cac cag ctg atg cta gac tgc tgg cag aag gag agg agc gac agg 2646  
Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp Arg  
855 860 865

cct aaa ttt ggg cag att gtc aac atg ttg gac aaa ctc atc cgc aac 2694  
Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn  
870 875 880

ccc aac agc ttg aag agg aca ggg acg gag agc tcc aga cct aac act 2742  
Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser Arg Pro Asn Thr  
885 890 895 900

gcc ttg ttg gat cca agc tcc cct gaa ttc tct gct gtc gta tca gtg 2790  
Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala Val Val Ser Val

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905	910	915	
ggc gat tgg ctc cag gcc att aaa atg gac cg <sup>g</sup> tat aag gat aac ttc Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr Lys Asp Asn Phe			2838
920	925	930	
935	940	945	2886
aca gct gct ggt tat acc aca cta gag gct gtg gtg cac gtg aac cag Thr Ala Ala Gly Tyr Thr Leu Glu Ala Val Val His Val Asn Gln			
950	955	960	2934
gag gac ctg gca aga att ggt atc aca gcc atc acg cac cag aat aag Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr His Gln Asn Lys			
965	970	975	980
			2982
att ttg agc agt gtc cag gca atg cga acc caa atg cag cag atg cac Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln Met His			
985			
ggc aga atg gtt ccc gtc tga gccagtactg aataaactca aaactcttga Gly Arg Met Val Pro Val			3033
aattagttta cctcatccat gcactttaat tgaagaactg cactttttt acttcgtctt	3093		
cgcctctga aattaaagaa atgaaaaaaaaaaa aaaacaatat ctgcagcg <sup>t</sup> gcttggtgca	3153		
cagattgctg aaactgtggg gcttacagaa atgactgccg gtcattt <sup>g</sup> tgagacctgg	3213		
aacaaatcgt ttctcagaag tactttctg ttcatcacca gtctgtaaaa tacatgtacc	3273		

1 2 / 3 2

tatagaaaata gaacactgcc tctgagttt gatgctgtat ttgctgccag acactgagct	3333
tctgagacat ccctgattct ctctccattt ggaattacaa ccattgtatt ttgtttgtgg	3393
cataaaattac agtcatctgt ctttcactgg aatgaagacc atgccttagga acattttta	3453
aggactcagc tgtgg	3468

&lt;210&gt; 2

&lt;211&gt; 986

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met Ala Gly Ile Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile			
1	5	10	15

Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr		
20	25	30

Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser		
35	40	45

Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn		
50	55	60

Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln			
65	70	75	80

1 3 / 3 2

Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg

85 90 95

Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro

100 105 110

Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu

115 120 125

Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys

130 135 140

Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly

145 150 155 160

Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu

165 170 175

Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile

180 185 190

Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val

195 200 205

Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser

1 4 / 3 2

210

215

220

Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys

225

230

235

240

Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro

245

250

255

Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu

260

265

270

Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala

275

280

285

Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala

290

295

300

Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala

305

310

315

320

Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile

325

330

335

Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln

340

345

350

1 5 / 3 2

Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys

355 360 365

Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val

370 375 380

His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile

385 390 395 400

Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val

405 410 415

Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val

420 425 430

Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln

435 440 445

Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro

450 455 460

Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu

465 470 475 480

Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg

485 490 495

1 6 / 3 2

Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His

500 505 510

Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu

515 520 525

Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala

530 535 540

Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val

545 550 555 560

Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr

565 570 575

Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly

580 585 590

Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala

595 600 605

Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu

610 615 620

Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu

1 7 / 3 2

625                  630                  635                  640

Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys

645                  650                  655

Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser

660                  665                  670

Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val

675                  680                  685

Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn

690                  695                  700

Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val

705                  710                  715                  720

Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr

725                  730                  735

Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile

740                  745                  750

Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser

755                  760                  765

1 8 / 3 2

Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly  
770                    775                    780

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys  
785                    790                    795                    800

Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu  
805                    810                    815

Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp  
820                    825                    830

Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp  
835                    840                    845

Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu  
850                    855                    860

Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys  
865                    870                    875                    880

Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser  
885                    890                    895

Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala  
900                    905                    910

1 9 / 3 2

Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr

915

920

925

Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val

930

935

940

His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr

945

950

955

960

His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met

965

970

975

Gln Gln Met His Gly Arg Met Val Pro Val

980

985

<210> 3

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificial synthesized primer sequence for RT-PCR

<400> 3

20 / 32

gaaggcgtgg tcactaaatg taa

23

&lt;210&gt; 4

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificial synthesized primer sequence for RT-PCR

&lt;400&gt; 4

tttaatttca gagggcgaag ac

22

&lt;210&gt; 5

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificially synthesized primer sequence for RT-PCR

&lt;400&gt; 5

catccacgaa actacaccttca act

23

2 1 / 3 2

<210> 6

<211> 23

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

<400> 6

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23

<210> 7

<211> 20

<212> DNA

<213> Artificial

<220>

<223> An artificial synthesized primer sequence for RT-PCR

<400> 7

caccccccact gaaaaagaga

20

<210> 8

2 2 / 3 2

<211> 19

<212> DNA

<213> Artificial

<220>

<223> An artificial synthesized primer sequence for RT-PCR

<400> 8

tacctgtgga gcaagggtgc

19

<210> 9

<211> 9

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized spacer sequence for siRNA

<400> 9

ttcaagaga

9

<210> 10

<211> 19

<212> DNA

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<213> Artificial

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<223> An artificial synthesized target sequence for siRNA

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gcagcaccat catccattg

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<210> 11

<211> 19

<212> DNA

<213> Artificial

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<223> An artificial synthesized target sequence for siRNA

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gaaggcagcac gacttcttc

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<210> 12

<211> 51

<212> DNA

<213> Artificial

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caccgcagca ccatcatcca ttgttcaaga gacaatggat gatggtgctg c 51

<210> 13

<211> 51

<212> DNA

<213> Artificial

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<223> An artificially synthesized sequence for siRNA

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aaaagcagca ccatcatcca ttgtcttttg aacaatggat gatggtgctg c 51

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<212> DNA

<213> Artificial

<220>

<223> siRNA hairpin design

25 / 32

&lt;400&gt; 14

gcagcaccat catccattgt tcaagagaca atggatgatg gtgctgc 47

&lt;210&gt; 15

&lt;211&gt; 4863

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; An artificially constructed plasmid sequence of siRNA expression vector.

&lt;400&gt; 15

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gcccgcgtct	gaaccctccg	cggccgcggc	gccccagtg	aaagacgcgc	aggcaaaacg	180
caccacgtga	cggagcgtga	ccgccccccg	agcgcgcgc	aaggtcgggc	aggaagaggg	240
cctatttccc	atgattcctt	catatttgca	tatacgatac	aaggctgtta	gagagataat	300
tagaattaat	ttgactgtaa	acacaaagat	attagtacaa	aatacgtgac	gtagaaagta	360
ataatttctt	ggtagtttg	cagttttaaa	attatgtttt	aaaatggact	atcatatgt	420
taccgttaact	tgaaagtatt	tcgatttctt	ggcttatat	atcttgtgga	aaggacgaaa	480
cacctttta	catcagggtt	ttttctgtt	tggttttttt	tttacaccac	gtttatacgc	540
cggtgcacgg	tttaccactg	aaaacacctt	tcatctacag	gtgatatctt	ttaacacaaa	600
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2 6 / 3 2

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